



#10

SEQUENCE LISTING

<110> Messier, Walter

Sikela, James M

<120> Methods to Identify Polynucleotide and Polypeptide
Sequences Which May Be Associated with Physiological
and Medical Conditions

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<150> 09/591,435

<151> 2000-06-09

<150> 09/240,915

<151> 1999-01-29

<150> 60/073,263

<151> 1998-01-30

<150> 60/098,987

<151> 1998-09-02

<150> 09/942,252

<151> 2001-08-28

<170> PatentIn Ver. 2.0

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Ile Glu Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Gly Gly Asn Asn

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Trp Gln Pro Val Gly Lys Asp Leu Thr Leu Arg Cys Gln Val Glu Gly	
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Gly Ala Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys	
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Glu Leu Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr	
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Gly Thr Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Arg	
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Glu Thr Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val	
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Ile Leu Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys	
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ccc cga ctg gac gag agg gat tgt ccg gga aac tgg acg tgg cca gaa	1152
Pro Arg Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu	
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<212> PRT

'<213> Pan troglodytes

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45

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Cys Tyr Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu
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Trp Gln Pro Val Gly Lys Asp Leu Thr Leu Arg Cys Gln Val Glu Gly
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Ser Ala Pro His Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro
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Asp Ser Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu
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Glu Thr Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val
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Ile Leu Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys
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Cys Glu Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala
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325 330 335

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340 345 350

Gln Leu Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly
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Pro Arg Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu
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Glu Leu Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Val Gly Glu
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Arg Ser Thr Gln Gly Glu Val Thr Arg Lys Val Thr Val Asn Val Leu
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Ser Pro Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Ala Val
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Ile Met Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg
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<212> DNA

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<212> PRT

<213> Homo sapiens

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Asp Ser Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu
245 250 255

Gly Thr Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln
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Ile Leu Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys
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Cys Glu Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala
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Gln Pro Leu Gly Pro Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu

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Glu Leu Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu		
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Arg Ser Thr Gln Gly Glu Val Thr Arg Glu Val Thr Val Asn Val Leu		
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Ile Met Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg		
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490

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Lys Pro Asn Thr Gln Ala Thr Pro Pro

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505

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<213> Homo sapiens

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20

25

30

Gln Pro Glu Val Gly Gly Leu Glu Thr Ser Leu Asp Lys Ile Leu Leu

35

40

45

Asp Glu Gln Ala Gln Trp Lys His Tyr Leu Val Ser Asn Ile Ser His

50

55

60

Asp Thr Val Leu Gln Cys His Phe Thr Cys Ser Gly Lys Gln Glu Ser

65

70

75

80

Met Asn Ser Asn Val Ser Val Tyr Gln Pro Pro Arg Gln Val Ile Leu

85

90

95

Thr Leu Gln Pro Thr Leu Val Ala Val Gly Lys Ser Phe Thr Ile Glu

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Ser Arg Gly Gly Asn Ile Phe His Lys His Ser Ala Pro Lys Met Leu					
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Glu Ile Tyr Glu Pro Val Ser Asp Ser Gln Met Val Ile Ile Val Thr					
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Phe Ile Phe Gly Gln His Leu Arg Gln Gln Arg Met Gly Thr Tyr Gly					
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35 40 45

Met Gly Trp Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser Arg

50 55 60

Ile Leu Cys Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser Ser

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Val	Tyr	Leu	Ala	Leu	Gly	Asp	Gln	Met	Leu	Asn	Ala	Thr	Val	Met	Asn
225															240
				230						235					
His	Gly	Asp	Thr	Leu	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Arg	Ala	Asp
				245						250					255
Gln	Glu	Gly	Ala	Arg	Glu	Ile	Val	Cys	Asn	Val	Thr	Leu	Gly	Gly	Glu
				260						265					270
Arg	Arg	Glu	Ala	Arg	Glu	Asn	Leu	Thr	Val	Phe	Ser	Phe	Leu	Gly	Pro
				275						280					285
Ile	Val	Asn	Leu	Ser	Glu	Pro	Thr	Ala	His	Glu	Gly	Ser	Thr	Val	Thr

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Pro Ala Ala Ala Pro Gly Gln Pro Ala Gln Leu Gln Leu Asn Ala Thr			
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Glu Ser Asp Asp Gly Arg Ser Phe Phe Cys Ser Ala Thr Leu Glu Val			
	340	345	350
Asp Gly Glu Phe Leu His Arg Asn Ser Ser Val Gln Leu Arg Val Leu			
	355	360	365
Tyr Gly Pro Lys Ile Asp Arg Ala Thr Cys Pro Gln His Leu Lys Trp			
	370	375	380
Lys Asp Lys Thr Arg His Val Leu Gln Cys Gln Ala Arg Gly Asn Pro			
385	390	395	400
Tyr Pro Glu Leu Arg Cys Leu Lys Glu Gly Ser Ser Arg Glu Val Pro			
	405	410	415
Val Gly Ile Pro Phe Phe Val Asn Val Thr His Asn Gly Thr Tyr Gln			
	420	425	430
Cys Gln Ala Ser Ser Ser Arg Gly Lys Tyr Thr Leu Val Val Val Met			
	435	440	445
Asp Ile Glu Ala Gly Ser Ser His Phe Val Pro Val Phe Val Ala Val			
	450	455	460

Leu Leu Thr Leu Gly Val Val Thr Ile Val Leu Ala Leu Met Tyr Val
465 470 475 480

Phe Arg Glu His Gln Arg Ser Gly Ser Tyr His Val Arg Glu Glu Ser
485 490 495

Thr Tyr Leu Pro Leu Thr Ser Met Gln Pro Thr Glu Ala Met Gly Glu
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Glu Pro Ser Arg Ala Glu
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<213> Homo sapiens

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<213> Pan troglodytes

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<213> Gorilla gorilla

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<211> 105

<212> PRT

<213> Pan troglodytes

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20 25 30

Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe

35 40 45

Asn Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys

50 55 60

Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly

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90

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Ala Ala Ala Ala Trp Ser Leu His Pro

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<211> 121

<212> PRT

<213> Pan troglodytes

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Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Leu Glu His Cys Asn Phe

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Lys Asp Leu Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys

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Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly

65

70

75

80

Asn Glu Gln Leu Glu Asn Gly Gly Asn Glu Gln Leu Glu Asn Gly Gly

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Thr Ser Leu Ser Glu Lys Thr Val Leu Leu Arg Val Thr Pro Phe Leu

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105

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Ala Ala Ala Ala Trp Ser Leu His Pro

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<211> 5140

<212> DNA

<213> Homo sapiens

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Met Gln

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Phe Leu Glu Glu Val Gln Pro Tyr Arg Ala Leu Lys His Ser Asn Leu

5

10

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Leu Gln Cys Leu Ala Gln Cys Ala Glu Val Thr Pro Tyr Leu Leu Val

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25

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atg gag ttc tgc cca ctg ggg gac ctc aag ggc tac ctg cgg agc tgc 562

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Thr Val Lys Ile Gly Asp Tyr Gly Leu Ala His Cys Lys Tyr Arg Glu

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110

gac tac ttc gtg act gcc gac cag ctg tgg gtg cct ctg cgc tgg atc 802

Asp Tyr Phe Val Thr Ala Asp Gln Leu Trp Val Pro Leu Arg Trp Ile

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120

125

130

gcg cca gag ctg gtg gac gag gtg cat agc aac ctg ctc gtc gtg gac	850
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Val Leu Ala Tyr Thr Val Arg Glu Gln Gln Leu Lys Leu Pro Lys Pro	
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Gln Leu Gln Leu Thr Leu Ser Asp Arg Trp Tyr Glu Val Met Gln Phe	
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Cys Trp Leu Gln Pro Glu Gln Arg Pro Thr Ala Glu Glu Val His Leu	
215 220 225	
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Leu Leu Ser Tyr Leu Cys Ala Lys Gly Ala Thr Glu Ala Glu Glu Glu	
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Phe Glu Arg Arg Trp Arg Ser Leu Arg Pro Gly Gly Gly Gly Val Gly	
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ccc ggg ccc ggt gcg gcg ggg ccc atg ctg ggc ggc gtg gtg gag ctc 1234
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260

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ttc cac gcg gac ggc gac gac gtg ctg acg gtg acc gag acc agc cga 1330
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295

300

305

ggc ctc aat ttt gag tac aag tgg gag gcg ggc cgc ggc gcg gag gcc 1378
 Gly Leu Asn Phe Glu Tyr Lys Trp Glu Ala Gly Arg Gly Ala Glu Ala

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 Phe Pro Ala Thr Leu Ser Pro Gly Arg Thr Ala Arg Leu Gln Glu Leu

325

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tgc gcc ccc gac ggc gcg ccc ccg ggc gtg gtt ccg gtg ctc agc gcg 1474
 Cys Ala Pro Asp Gly Ala Pro Pro Gly Val Val Pro Val Leu Ser Ala

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 His Ser Pro Ser Leu Gly Ser Glu Tyr Phe Ile Arg Leu Glu Glu Ala

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360

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gca ccc gcc gcc ggc cac gac cct gac tgc gcc ggc tgc gcc ccc agt 1570

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cca cct gcc acc gcg gac cag gac gac gac tct gac ggc agc acc gcc	1618
Pro Pro Ala Thr Ala Asp Gln Asp Asp Asp Ser Asp Gly Ser Thr Ala	
390 395 400	
gcc tcg ctg gcc atg gag ccg ctg ctg ggc cac ggg cca ccc gtc gac	1666
Ala Ser Leu Ala Met Glu Pro Leu Leu Gly His Gly Pro Pro Val Asp	
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Val Pro Trp Gly Arg Gly Asp His Tyr Pro Arg Arg Ser Leu Ala Arg	
420 425 430	
gac ccg ctc tgc ccc tca cgc tct ccc tcg ccc tcg gcg ggc ccc ctg	1762
Asp Pro Leu Cys Pro Ser Arg Ser Pro Ser Pro Ser Ala Gly Pro Leu	
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Ser Leu Ala Glu Gly Gly Ala Glu Asp Ala Asp Trp Gly Val Ala Ala	
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Phe Cys Pro Ala Phe Phe Glu Asp Pro Leu Gly Thr Ser Pro Leu Gly	
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Ser Ser Gly Ala Pro Pro Leu Pro Leu Thr Gly Glu Asp Glu Leu Glu	
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Glu Val Gly Ala Arg Arg Ala Ala Gln Arg Gly His Trp Arg Ser Asn	
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Val Ser Ala Asn Asn Asn Ser Gly Ser Arg Cys Pro Glu Ser Trp Asp	
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Pro Val Ser Ala Gly Cys His Ala Glu Gly Cys Pro Ser Pro Lys Gln	
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acc cca cgg gcc tcc ccc gag ccg ggg tac cct gga gag cct ctg ctt	2098
Thr Pro Arg Ala Ser Pro Glu Pro Gly Tyr Pro Gly Glu Pro Leu Leu	
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Gly Leu Gln Ala Ala Ser Ala Gln Glu Pro Gly Cys Cys Pro Gly Leu	
565 570 575	
cct cat cta tgc tct gcc cag ggc ctg gca cct gct ccc tgc ctg gtt	2194
Pro His Leu Cys Ser Ala Gln Gly Leu Ala Pro Ala Pro Cys Leu Val	
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aca ccc tcc tgg aca gag aca gcc agt agt ggg ggt gac cac ccg cag	2242
Thr Pro Ser Trp Thr Glu Thr Ala Ser Ser Gly Gly Asp His Pro Gln	
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gca gag ccc aag ctt gcc acg gag gct gag ggc act acc gga ccc cgc	2290
Ala Glu Pro Lys Leu Ala Thr Glu Ala Glu Gly Thr Thr Gly Pro Arg	

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Leu Pro Leu Pro Ser Val Pro Ser Pro Ser Gln Glu Gly Ala Pro Leu			
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ccc tcg gag gag gcc agt gcc ccc gac gcc cct gat gcc ctg cct gac			2386
Pro Ser Glu Glu Ala Ser Ala Pro Asp Ala Pro Asp Ala Leu Pro Asp			
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tct ccc acg cct gct act ggt ggc gag gtg tct gcc atc aag ctg gct			2434
Ser Pro Thr Pro Ala Thr Gly Gly Glu Val Ser Ala Ile Lys Leu Ala			
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Ser Ala Leu Asn Gly Ser Ser Ser Ser Pro Glu Val Glu Ala Pro Ser			
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Ser Glu Asp Glu Asp Thr Ala Glu Ala Thr Ser Gly Ile Phe Thr Asp			
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Thr Ser Ser Asp Gly Leu Gln Ala Arg Arg Pro Asp Val Val Pro Ala			
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Phe Arg Ser Leu Gln Lys Gln Val Gly Thr Pro Asp Ser Leu Asp Ser			
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ctg gac atc ccg tcc tca gcc agt gat ggt ggc tat gag gtc ttc agc			2674

Leu Asp Ile Pro Ser Ser Ala Ser Asp Gly Gly Tyr Glu Val Phe Ser	
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Pro Ser Ala Thr Gly Pro Ser Gly Gly Gln Pro Arg Ala Leu Asp Ser	
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Gln Lys Arg Met Gly Gly Pro Gly Thr Pro Arg Ala Pro Leu Arg Leu	
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Tyr Ser Val Gln Glu Pro Ser Glu Asp Ser Glu Glu Glu Ala Pro Ala

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Glu Ser Lys Glu Ala

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35 40 45

Ser Cys Arg Val Ala Glu Ser Met Ala Pro Asp Pro Arg Thr Leu Gln

50 55 60

Arg Met Ala Cys Glu Val Ala Cys Gly Val Leu His Leu His Arg Asn

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Trp Glu Leu Phe Glu Leu Gly Thr Gln Pro Tyr Pro Gln His Ser Asp
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Gln Gln Val Leu Ala Tyr Thr Val Arg Glu Gln Gln Leu Lys Leu Pro
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Lys Pro Gln Leu Gln Leu Thr Leu Ser Asp Arg Trp Tyr Glu Val Met
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Gln Phe Cys Trp Leu Gln Pro Glu Gln Arg Pro Thr Ala Glu Glu Val
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His Leu Leu Leu Ser Tyr Leu Cys Ala Lys Gly Ala Thr Glu Ala Glu
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Glu Glu Phe Glu Arg Arg Trp Arg Ser Leu Arg Pro Gly Gly Gly Gly
 245 250 255

Val Gly Pro Gly Pro Gly Ala Ala Gly Pro Met Leu Gly Gly Val Val
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Glu Leu Ala Ala Ala Ser Ser Phe Pro Leu Leu Glu Gln Phe Ala Gly

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Asp Gly Phe His Ala Asp Gly Asp Asp Val Leu Thr Val Thr Glu Thr

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Ser Arg Gly Leu Asn Phe Glu Tyr Lys Trp Glu Ala Gly Arg Gly Ala

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Glu Ala Phe Pro Ala Thr Leu Ser Pro Gly Arg Thr Ala Arg Leu Gln

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330

335

Glu Leu Cys Ala Pro Asp Gly Ala Pro Pro Gly Val Val Pro Val Leu

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Ser Ala His Ser Pro Ser Leu Gly Ser Glu Tyr Phe Ile Arg Leu Glu

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360

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Glu Ala Ala Pro Ala Ala Gly His Asp Pro Asp Cys Ala Gly Cys Ala

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375

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Pro Ser Pro Pro Ala Thr Ala Asp Gln Asp Asp Asp Ser Asp Gly Ser

385

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Val Asp Val Pro Trp Gly Arg Gly Asp His Tyr Pro Arg Arg Ser Leu

420

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Ala Arg Asp Pro Leu Cys Pro Ser Arg Ser Pro Ser Pro Ser Ala Gly

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440

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Pro Leu Ser Leu Ala Glu Gly Gly Ala Glu Asp Ala Asp Trp Gly Val

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Ala Ala Phe Cys Pro Ala Phe Phe Glu Asp Pro Leu Gly Thr Ser Pro

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510

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Lys Gln Thr Pro Arg Ala Ser Pro Glu Pro Gly Tyr Pro Gly Glu Pro

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Lys Glu Ala Gln Glu Gly Cys Glu Pro Gln Ala Phe Ala Glu Leu Ala
785 790 795 800

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Ser Gly Leu Asn Glu Lys Asn Pro Tyr Arg Asp Ser Ala Tyr Phe Ser
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Gly Gly Asp Arg Ala Pro Gly Pro Glu Leu Gly Leu Pro Ser Thr Gly
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Pro Pro Glu Pro Gln Gly Pro Ala Lys Val Arg Pro Gly Pro Ser Pro
915 920 925

Ser Cys Ser Gln Phe Phe Leu Leu Thr Pro Val Pro Leu Arg Ser Glu
930 935 940

Gly Asn Ser Ser Glu Phe Gln Gly Pro Pro Gly Leu Leu Ser Gly Pro
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Ala Pro Gln Lys Arg Met Gly Gly Pro Gly Thr Pro Arg Ala Pro Leu
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Arg Leu Ala Leu Pro Gly Leu Pro Ala Ala Leu Glu Gly Arg Pro Glu
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Glu Glu Glu Glu Asp Ser Glu Asp Ser Asp Glu Ser Asp Glu Glu Leu
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Arg Cys Tyr Ser Val Gln Glu Pro Ser Glu Asp Ser Glu Glu Glu Ala
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Pro Ala Val Pro Val Val Val Ala Glu Ser Gln Ser Ala Arg Asn Leu
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Val Tyr Leu Phe Asp Gln Glu Ser Pro Thr Arg Glu Leu Gly Glu Pro
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<213> Gorilla gorilla

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ggcgagggcc ccgggccc

18

<210> 22

<211> 24

<212> DNA

<213> Pan troglodytes

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ctggaggctg aggccgaggc cgag

24

<210> 23

<211> 18

<212> DNA

<213> Homo sapiens

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ctcgaggctg aggccgag

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<212> DNA

<213> Gorilla gorilla

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ctggaggctg aggccgag

18

<210> 25

<211> 18

<212> DNA

<213> Pan troglodytes

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cccacgcccg ctcccttc

18

<210> 26

<211> 24

<212> DNA

<213> Homo sapiens

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cccacgcca cgcccgtcc ctcc

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<212> DNA

<213> Gorilla gorilla

<400> 27

cccacgcccg ctcccttc

18

<210> 28

<211> 24

<212> DNA

<213> Pan troglodytes

<400> 28

cccacgtcca cgtcccgtt ctcc

24

<210> 29

<211> 18

<212> DNA

<213> Homo sapiens

<400> 29

cccacgtccc gcttctcc

18

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<211> 18

<212> DNA

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<400> 30

cccacgtccc gcttctcc

18

<210> 31

<211> 1335

<212> DNA

<213> Pan troglodytes

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cttgacagat gttgtaatca agggcctact ctaacagtga tttatagtga agatcatatt 180

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gcacttcaag agactaaaat ttcagaatgg aaactaggac tatatacacc agaaacactg 300

ttttgttg acgttgcaaa atataactcc ccaactaatt tccagataga tggaagaaat 360

agaaaagtga ttatggactt aaagacaatg gaaaatcttg gacttgctca aaattgtact 420

atctctattc aggattatga agtttttcga tgcgaagatt cactggacga aagaaagata 480

aaaggggtca ttgagctcag gaagagctta ctgtctgcct tgagaactta tgaaccatat 540

ggatccctgg ttcaacaaat acgaattctg ctgctgggtc caattggagc tgggaagtct 600

agctttttca actcagtga gtcgtttttc caagggcatg taacgcatca ggctttggtg 660

ggcactaata caactgggat atctgagaag tataggacat actctattag agacgggaaa 720

gatggcaa at acctgccatt tattctgtgt gactcactgg ggctgagtga gaaagaaggc 780

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aaggacagaa ttcattgtgt ggcatttgta tttgatgcc a gctctattga atacttctcc 960
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gtaaaggatg ttctaattct ttctgctctg agacgaatgc tatgggctgc agatgacttc 1260
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caaggaaaaa aatag 1335

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<211> 1335

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<220>

<221> Variation

<222> 212

<223> M= A or C

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Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

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aat cat ttt gga ggg aag cgg ctt agc ctt ctc tat aag ggt agt gtc				96
Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val				
	20	25	30	
cat gga ttc cat aat gga gtt ttg ctt gac aga tgt tgt aat caa ggg				144
His Gly Phe His Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly				
	35	40	45	
cct act cta aca gtg att tat agt gaa gat cat att att gga gca tat				192
Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr				
	50	55	60	
gca gaa gag ggt tac cag gma aga aag tat gct tcc atc atc ctt ttt				240
Ala Glu Glu Gly Tyr Gln Xaa Arg Lys Tyr Ala Ser Ile Ile Leu Phe				
65	70	75	80	
gca ctt caa gag act aaa att tca gaa tgg aaa cta gga cta tat aca				288
Ala Leu Gln Glu Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Tyr Thr				
	85	90	95	
cca gaa aca ctg ttt tgt tgt gac gtt gca aaa tat aac tcc cca act				336
Pro Glu Thr Leu Phe Cys Cys Asp Val Ala Lys Tyr Asn Ser Pro Thr				
	100	105	110	
aat ttc cag ata gat gga aga aat aga aaa gtg att atg gac tta aag				384
Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys				
	115	120	125	

aca atg gaa aat ctt gga ctt gct caa aat tgt act atc tct att cag	432
Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln	
130 135 140	
 gat tat gaa gtt ttt cga tgc gaa gat tca ctg gac gaa aga aag ata	480
Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile	
145 150 155 160	
 aaa ggg gtc att gag ctc agg aag agc tta ctg tct gcc ttg aga act	528
Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr	
165 170 175	
 tat gaa cca tat gga tcc ctg gtt caa caa ata cga att ctg ctg ctg	576
Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu	
180 185 190	
 ggg cca att gga gct ggg aag tct agc ttt ttc aac tca gtg agg tct	624
Gly Pro Ile Gly Ala Gly Lys Ser Ser Phe Phe Asn Ser Val Arg Ser	
195 200 205	
 gtt ttc caa ggg cat gta acg cat cag gct ttg gtg ggc act aat aca	672
Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr	
210 215 220	
 act ggg ata tct gag aag tat agg aca tac tct att aga gac ggg aaa	720
Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys	
225 230 235 240	
 gat ggc aaa tac ctg cca ttt att ctg tgt gac tca ctg ggg ctg agt	768
Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser	
245 250 255	

gag aaa gaa ggc ggc ctg tgc atg gat gac ata tcc tac atc ttg aac	816
Glu Lys Glu Gly Gly Leu Cys Met Asp Asp Ile Ser Tyr Ile Leu Asn	
260 265 270	
ggt aac att cgt gat aga tac cag ttt aat ccc atg gaa tca atc aaa	864
Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys	
275 280 285	
tta aat cat cat gac tac att gat tcc cca tgc ctg aag gac aga att	912
Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile	
290 295 300	
cat tgt gtg gca ttt gta ttt gat gcc agc tct att gaa tac ttc tcc	960
His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Glu Tyr Phe Ser	
305 310 315 320	
tct cag atg ata gta aag atc aaa aga att cga agg gag ttg gta aac	1008
Ser Gln Met Ile Val Lys Ile Lys Arg Ile Arg Arg Glu Leu Val Asn	
325 330 335	
gct ggt gtg gta cat gtg gct ttg ctc act cat gtg gat agc atg gat	1056
Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp	
340 345 350	
ctg att aca aaa ggt gac ctt ata gaa ata gag aga tgt gtg cct gtg	1104
Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Val Pro Val	
355 360 365	
agg tcc aag cta gag gaa gtc caa aga aaa ctt gga ttt gct ctt tct	1152

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

gac atc tcg gtg gtt agc aat tat tcc tct gag tgg gag ctg gac cct 1200

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400

gta aag gat gtt cta att ctt tct gct ctg aga cga atg cta tgg gct 1248

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

gca gat gac ttc tta gag gat ttg cct ttt gag caa ata ggg aat cta 1296

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

agg gag gaa att atc aac tgt gca caa gga aaa aaa tag

1335

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440

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<212> PRT

<213> Pan troglodytes

<220>

<221> Variation

<222> 71

<223> Xaa= Glu or Ala

<400> 33

Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

1

5

10

15

Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

20

25

30

His Gly Phe His Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly

35

40

45

Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr

50

55

60

Ala Glu Glu Gly Tyr Gln Xaa Arg Lys Tyr Ala Ser Ile Ile Leu Phe

65

70

75

80

Ala Leu Gln Glu Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Tyr Thr

85

90

95

Pro Glu Thr Leu Phe Cys Cys Asp Val Ala Lys Tyr Asn Ser Pro Thr

100

105

110

Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys

115

120

125

Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln

130

135

140

Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile

145

150

155

160

Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr

165

170

175

Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu
180 185 190

Gly Pro Ile Gly Ala Gly Lys Ser Ser Phe Phe Asn Ser Val Arg Ser
195 200 205

Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr
210 215 220

Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys
225 230 235 240

Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser
245 250 255

Glu Lys Glu Gly Gly Leu Cys Met Asp Asp Ile Ser Tyr Ile Leu Asn
260 265 270

Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys
275 280 285

Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile
290 295 300

His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Glu Tyr Phe Ser
305 310 315 320

Ser Gln Met Ile Val Lys Ile Lys Arg Ile Arg Arg Glu Leu Val Asn
325 330 335

Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp

340

345

350

Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Val Pro Val

355

360

365

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440

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<211> 1335

<212> DNA

<213> Homo sapiens

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cttgacagat gttgtaatca agggcctact ctaacagtga tttatagtga agatcatatt 180

attggagcat atgcagaaga gagttaccag gaaggaaagt atgcttccat catccttttt 240

gcacttcaag atactaaaat ttcagaatgg aaactaggac tatgtacacc agaaacactg 300

ttttgttgatg atgttacaaa atataactcc ccaactaatt tccagataga tggaagaaat 360

agaaaagtga ttatggactt aaagacaatg gaaaatcttg gacttgctca aaattgtact 420

atctctattc aggattatga agtttttcga tgcgaagatt cactggatga aagaaagata 480

aaaggggtca ttgagctcag gaagagctta ctgtctgcct tgagaactta tgaaccatat 540

ggatccctgg ttcaacaaat acgaattctc ctctgggtc caattggagc tcccaagtcc 600

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gatggcaaat acctgccgtt tattctgtgt gactcactgg ggctgagtga gaaagaaggc 780

ggcctgtgca gggatgacat attctatata ttgaacggtg acattcgtga tagataccag 840

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catgtggcctt tgctcactca tgtggatagc atggatttga ttacaaaagg tgaccttata 1080

gaaatagaga gatgtgagcc tgtgaggtcc aagctagagg aagtccaaag aaaacttgga 1140

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gtaaaggatg ttctaattct ttctgctctg agacgaatgc tatgggctgc agatgacttc 1260

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caaggaaaaa aatag 1335

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<211> 1335

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<213> Homo sapiens

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5

10

15

aat cat ttt gga ggg aag cgg ctt agc ctt ctc tat aag ggt agt gtc 96

Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

20

25

30

cat gga ttc cgt aat gga gtt ttg ctt gac aga tgt tgt aat caa ggg 144

His Gly Phe Arg Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly

35

40

45

cct act cta aca gtg att tat agt gaa gat cat att att gga gca tat 192

Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr

50

55

60

gca gaa gag agt tac cag gaa gga aag tat gct tcc atc atc ctt ttt 240

Ala Glu Glu Ser Tyr Gln Glu Gly Lys Tyr Ala Ser Ile Ile Leu Phe

65

70

75

80

gca ctt caa gat act aaa att tca gaa tgg aaa cta gga cta tgt aca 288

Ala Leu Gln Asp Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Cys Thr

85

90

95

cca gaa aca ctg ttt tgt tgt gat gtt aca aaa tat aac tcc cca act 336

Pro Glu Thr Leu Phe Cys Cys Asp Val Thr Lys Tyr Asn Ser Pro Thr

100

105

110

aat ttc cag ata gat gga aga aat aga aaa gtg att atg gac tta aag 384

Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys

115

120

125

aca atg gaa aat ctt gga ctt gct caa aat tgt act atc tct att cag 432

Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln

130

135

140

gat tat gaa gtt ttt cga tgc gaa gat tca ctg gat gaa aga aag ata 480

Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile
 145 150 155 160

aaa ggg gtc att gag ctc agg aag agc tta ctg tct gcc ttg aga act 528
 Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr
 165 170 175

tat gaa cca tat gga tcc ctg gtt caa caa ata cga att ctc ctc ctg 576
 Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu
 180 185 190

ggt cca att gga gct ccc aag tcc agc ttt ttc aac tca gtg agg tct 624
 Gly Pro Ile Gly Ala Pro Lys Ser Ser Phe Phe Asn Ser Val Arg Ser
 195 200 205

gtt ttc caa ggg cat gta acg cat cag gct ttg gtg ggc act aat aca 672
 Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr
 210 215 220

act ggg ata tct gag aag tat agg aca tac tct att aga gac ggg aaa 720
 Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys
 225 230 235 240

gat ggc aaa tac ctg ccg ttt att ctg tgt gac tca ctg ggg ctg agt 768
 Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser
 245 250 255

gag aaa gaa ggc ggc ctg tgc agg gat gac ata ttc tat atc ttg aac 816
 Glu Lys Glu Gly Gly Leu Cys Arg Asp Asp Ile Phe Tyr Ile Leu Asn
 260 265 270

ggt aac att cgt gat aga tac cag ttt aat ccc atg gaa tca atc aaa 864

Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys

275

280

285

tta aat cat cat gac tac att gat tcc cca tcg ctg aag gac aga att 912

Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile

290

295

300

cat tgt gtg gca ttt gta ttt gat gcc agc tct att caa tac ttc tcc 960

His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Gln Tyr Phe Ser

305

310

315

320

tct cag atg ata gta aag atc aaa aga att caa agg gag ttg gta aac 1008

Ser Gln Met Ile Val Lys Ile Lys Arg Ile Gln Arg Glu Leu Val Asn

325

330

335

gct ggt gtg gta cat gtg gct ttg ctc act cat gtg gat agc atg gat 1056

Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp

340

345

350

ttg att aca aaa ggt gac ctt ata gaa ata gag aga tgt gag cct gtg 1104

Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Glu Pro Val

355

360

365

agg tcc aag cta gag gaa gtc caa aga aaa ctt gga ttt gct ctt tct 1152

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

gac atc tcg gtg gtt agc aat tat tcc tct gag tgg gag ctg gac cct 1200

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400,

gta aag gat gtt cta att ctt tct gct ctg aga cga atg cta tgg gct 1248

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

gca gat gac ttc tta gag gat ttg cct ttt gag caa ata ggg aat cta 1296

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

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1335

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440

<210> 36

<211> 444

<212> PRT

<213> Homo sapiens

<400> 36

Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

1

5

10

15

Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

20

25

30

His Gly Phe Arg Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly

35

40

45

Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr

50

55

60

Ala Glu Glu Ser Tyr Gln Glu Gly Lys Tyr Ala Ser Ile Ile Leu Phe

65

70

75

80

Ala Leu Gln Asp Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Cys Thr

85

90

95

Pro Glu Thr Leu Phe Cys Cys Asp Val Thr Lys Tyr Asn Ser Pro Thr

100

105

110

Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys

115

120

125

Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln

130

135

140

Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile

145

150

155

160

Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr

165

170

175

Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu

180

185

190

Gly Pro Ile Gly Ala Pro Lys Ser Ser Phe Phe Asn Ser Val Arg Ser

195

200

205

Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr

210

215

220

Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys

225

230

235

240

Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser

245

250

255

Glu Lys Glu Gly Gly Leu Cys Arg Asp Asp Ile Phe Tyr Ile Leu Asn

260

265

270

Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys

275

280

285

Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile

290

295

300

His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Gln Tyr Phe Ser

305

310

315

320

Ser Gln Met Ile Val Lys Ile Lys Arg Ile Gln Arg Glu Leu Val Asn

325

330

335

Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp

340

345

350

Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Glu Pro Val

355

360

365

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440